

Serial Number:

09/819047A

0570

#9

CRF Processing Date: 11/19/01

Edited by: MIA

Verified by:

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line

☐

Edited a format error in the Current Application Data section, specifically:

☐

Edited the Current Application Data section with the actual current number. The number input applicant was ☐ the prior application data; or ☐ other

☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited

☒

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

SEQ ID NOs 1 through 8

☐

Corrected subheading placement. All responses must be on the same line as each subheading applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

ENTERED

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☒

Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename a ☐ page numbers throughout text; ☐ other invalid text, such as

☐

Inserted mandatory headings, specifically:

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field according due to a PatentIn bug). Sequences corrected:

☐

Other:

*Examiner: The above corrections must be communicated to the applicant in the first Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING

DATE: 11/19/2001

PATENT APPLICATION: US/09/814,047A

TIME: 09:43:14

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\11192001\I814047A.raw

3 <110> APPLICANT: WAKAMATSU, Yuko
 4 OZATO, Kenjiro
 6 <120> TITLE OF INVENTION: SEE-THROUGH MEDAKA
 8 <130> FILE REFERENCE: 04853-0066-00000
 10 <140> CURRENT APPLICATION NUMBER: 09/814,047A
 11 <141> CURRENT FILING DATE: 2001-03-22
 W--> 13 <150> PRIOR APPLICATION NUMBER:
 W--> 14 <151> PRIOR FILING DATE:
 16 <160> NUMBER OF SEQ ID NOS: 8
 18 <170> SOFTWARE: PatentIn Ver. 2.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 25
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Oryzias latipes
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Forward primer pH05.5-F.
 28 <400> SEQUENCE: 1
 29 cctgcaatgg gaaattattc tgctc 25
 31 <210> SEQ ID NO: 2
 32 <211> LENGTH: 28
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Oryzias latipes
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: Reverse primer pH05.5-RV.
 39 <400> SEQUENCE: 2
 40 cttttgtgtc tttggttatg aaacgatg 28
 42 <210> SEQ ID NO: 3
 43 <211> LENGTH: 19
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Unknown
 47 <220> FEATURE:
 48 <221> NAME/KEY: modified_base
 49 <222> LOCATION: (6), (12), (18)
 50 <223> OTHER INFORMATION: represents a, g, t, or c OK
 51 <223> OTHER INFORMATION: Common sequence found in animals. The sequence is used
 52 herein as a forward primer to amplify the short fragment of
 53 vasa cDNA.
 55 <400> SEQUENCE: 3
 W--> 56 atggcntgyg cncaracng 19
 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 18
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Unknown
 63 <220> FEATURE:
 64 <221> NAME/KEY: modified_base
 65 <222> LOCATION: (4)
 66 <223> OTHER INFORMATION: represents a, g, t, or c OK

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/814,047A

DATE: 11/19/2001
TIME: 09:43:14

Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\11192001\I814047A.raw

67 <223> OTHER INFORMATION: Common sequence found in animals. The sequence is used
68 herein as a reverse primer used to amplify the short fragment
69 of vasa cDNA.
71 <400> SEQUENCE: 4
W--> 72 raancccatr tcyaacat 18
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 20
76 <212> TYPE: DNA
77 <213> ORGANISM: Oryzias latipes
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Primer T7 used to amplify the 3'region of vasa gene.
82 <400> SEQUENCE: 5
83 taatacgact cactataggg 20
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 23
87 <212> TYPE: DNA
88 <213> ORGANISM: Oryzias latipes
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Other information: Primer VI-8 used to amplify the
92 3'region of vasa gene.
94 <400> SEQUENCE: 6
95 aggaggtgcc gtcattggctg gag 23
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 30
99 <212> TYPE: DNA
100 <213> ORGANISM: Oryzias latipes
102 <220> FEATURE:
103 <223> OTHER INFORMATION: Other information: Primer VP1M used to amplify 5.1 kb
104 genomic fragment comprising the promotor region of vasa gene.
106 <400> SEQUENCE: 7
107 cctcccagtc gtccatatga atcgtctgat 30
109 <210> SEQ ID NO: 8
110 <211> LENGTH: 37
111 <212> TYPE: DNA
112 <213> ORGANISM: Oryzias latipes
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Other information: Primer VP3 used to amplify 5.1 kb
116 genomic fragment comprising the promotor region of vasa gene.
118 <400> SEQUENCE: 8
119 agaggatcca atagaatgag taatggttct ctatttc 37

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/814,047A

DATE: 11/19/2001

TIME: 09:43:15

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\11192001\I814047A.raw

L:13 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

RAW SEQUENCE LISTING

DATE: 11/16/2001

PATENT APPLICATION: US/09/814,047A

TIME: 08:04:10

Input Set : A:\es.txt

Output Set: N:\CRF3\11162001\I814047A.raw

3 <110> APPLICANT: WAKAMATSU, Yuko
 4 OZATO, Kenjiro
 6 <120> TITLE OF INVENTION: SEE-THROUGH MEDAKA
 8 <130> FILE REFERENCE: 04853-0066-00000
 10 <140> CURRENT APPLICATION NUMBER: 09/814,047A
 11 <141> CURRENT FILING DATE: 2001-03-22
 W--> 13 <150> PRIOR APPLICATION NUMBER:
 W--> 14 <151> PRIOR FILING DATE:
 16 <160> NUMBER OF SEQ ID NOS: 8
 18 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 25
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Oryzias latipes
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Forward primer phO5.5-F.
 28 <400> SEQUENCE: 1
 E--> 29 cctgcaatgg gaaattattc tgctc *→ move end of lone nucleotide*
 30 25
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 28
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Oryzias latipes
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Reverse primer phO5.5-RV.
 40 <400> SEQUENCE: 2
 E--> 41 cttttgtgtc ttggttatg aaacgatg *→ cause counter must move to end of loop*
 42 28
 44 <210> SEQ ID NO: 3
 45 <211> LENGTH: 19
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Unknown
 49 <220> FEATURE:
 50 <221> NAME/KEY: modified_base
 51 <222> LOCATION: (6), (12), (18)
 52 <223> OTHER INFORMATION: represents a, g, t, or c
 53 <223> OTHER INFORMATION: Common sequence found in animals. The sequence is used
 54 herein as a forward primer to amplify the short fragment of
 55 vasa cDNA.
 57 <400> SEQUENCE: 3
 E--> 58 atggcntgyg cncaracng *→ counter must move to end of loop*
 59 19
 61 <210> SEQ ID NO: 4

RAW SEQUENCE LISTING

DATE: 11/16/2001

PATENT APPLICATION: US/09/814,047A

TIME: 08:04:10

Input Set : A:\es.txt

Output Set: N:\CRF3\11162001\I814047A.raw

62 <211> LENGTH: 18
63 <212> TYPE: DNA
64 <213> ORGANISM: Unknown
66 <220> FEATURE:
67 <221> NAME/KEY: modified_base
68 <222> LOCATION: (4)
69 <223> OTHER INFORMATION: represents a, g, t, or c
70 <223> OTHER INFORMATION: Common sequence found in animals. The sequence is used
71 herein as a reverse primer used to amplify the short fragment
72 of vasa cDNA.

74 <400> SEQUENCE: 4
E--> 75 raancccatr tcyaacat → counter must move to end of line

76 18
78 <210> SEQ ID NO: 5
79 <211> LENGTH: 20
80 <212> TYPE: DNA
81 <213> ORGANISM: Oryzias latipes
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Primer T7 used to amplify the 3' region of vasa gene.
86 <400> SEQUENCE: 5

E--> 87 taatagcact cactataggg → counter must move to end of line

88 20
90 <210> SEQ ID NO: 6
91 <211> LENGTH: 23
92 <212> TYPE: DNA
93 <213> ORGANISM: Oryzias latipes
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Other information: Primer VI-8 used to amplify the
97 3' region of vasa gene.
99 <400> SEQUENCE: 6

E--> 100 aggaggtgcc gtcattgctg gag → move counter to end of line

101 23
103 <210> SEQ ID NO: 7
104 <211> LENGTH: 30
105 <212> TYPE: DNA
106 <213> ORGANISM: Oryzias latipes
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Other information: Primer VP1M used to amplify 5.1 kb
110 genomic fragment comprising the promotor region of vasa gene.
112 <400> SEQUENCE: 7

E--> 113 cctcccagtc gtccatatga atcgtctgat →

114 30
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 37
118 <212> TYPE: DNA
119 <213> ORGANISM: Oryzias latipes
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Other information: Primer VP3 used to amplify 5.1 kb
123 genomic fragment comprising the promotor region of vasa gene.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/814,047A

DATE: 11/16/2001

TIME: 08:04:10

Input Set : A:\es.txt

Output Set: N:\CRF3\11162001\I814047A.raw

125 <400> SEQUENCE: 8

E--> 126 agaggatcca atagaatgag taatggttct ctatttc

127 37

E--> 130 (1/1) *delete End of file N-ABCT test*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/814,047A

DATE: 11/16/2001

TIME: 08:04:11

Input Set : A:\es.txt

Output Set: N:\CRF3\11162001\I814047A.raw

L:13 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
 L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
 L:29 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:1
 L:41 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:2
 L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:58 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:3
 L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:75 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:4
 L:87 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:5
 L:100 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:6
 L:113 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:7
 L:126 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:37 SEQ:8
 M:254 Repeated in SeqNo=8
 L:130 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 L:130 M:252 E: No. of Seq. differs, <211>LENGTH:Input:37 Found:38 SEQ:8

STATISTICS SUMMARY

PATENT APPLICATION: US/09/814,047A

DATE: 11/16/2001

TIME: 08:04:11

Input Set : A:\es.txt

Output Set: N:\CRF3\11162001\I814047A.raw

Application Serial Number: US/09/814,047A

Alpha or Numeric: Numeric

Application Class:

Application File Date: 03-22-2001

Art Unit: OIPE

Software Application: PatentIn

Total Number of Sequences: 8

Total Nucleotides: 201

Total Amino Acids: 0

Number of Errors: 11

Number of Warnings: 4

Number of Corrections: 0

MESSAGE SUMMARY

252 E: 1 (No. of Seq. differs)

254 E: 9 (No. of Bases conflict)

256 W: 2 (Invalid Numeric Header Field)

320 E: 1 ((1) Wrong Nucleic Acid Designator)

341 W: 2 ((46) "n" or "Xaa" used)

*Patn 20
NE - Edit*